

#6

SEQUENCE LISTING

<110> Moon, The Hwan Chen, Lingjing Sung, Zinmay R.

<120> NUCLEIC ACIDS THAT CONTROL REPRODUCTIVE DEVELOPMENT IN PLANTS

<130> 018941-001400US

<140> 09/828,068

<141> 2001-04-06

<160> 2

<170> PatentIn Ver. 2.1

<210> 1

<211> 3896

<212> DNA

<213> Oryza sativa

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<222> (241)..(3411)

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atg gag att gtt gca gta gat cag gag gga gct cgt gtt ggg acg 288 Met Glu Ile Val Ala Val Asp Gln Glu Gly Ala Arg Val Val Gly Thr 1 5 10 15

aac tgt atg ctt gct cgt ggt gga act ggt gct gta gcg cca gtg ttg 336 Asn Cys Met Leu Ala Arg Gly Gly Thr Gly Ala Val Ala Pro Val Leu 20 25 30

gag ctg aca gcg acg cct cgt cag gat gca gcc gct gaa gct ggt gta 384 Glu Leu Thr Ala Thr Pro Arg Gln Asp Ala Ala Ala Glu Ala Gly Val 35 40 45

gac gaa ccg gca caa cac caa tgc gag cat ttc tcc ata aga ggg tat 432 Asp Glu Pro Ala Gln His Gln Cys Glu His Phe Ser Ile Arg Gly Tyr

gtt gct ctt ctt cag aag aag gat cca aaa ttc tgc tct cta tct cgg 480 Val Ala Leu Leu Gln Lys Lys Asp Pro Lys Phe Cys Ser Leu Ser Arg 65 70 75 80

att ttc cat gac cag aaa aaa tgt gat gaa cac aaa gct agt tca agc 528

Ile Phe His Asp Gln Lys Lys Cys Asp Glu His Lys Ala Ser Ser Ser

85 90 95

							cga Arg									576
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							gat Asp									672
							gtt Val									720
							aat Asn									768
agt Ser	gtg Val	caa Gln	gaa Glu 180	ggc Gly	aat Asn	gac <u>A</u> sp	tcc Ser	aaa L <u>y</u> s 185	tgc Cys	aat Asn	gcg Ala	cct Pro	tct Ser 190	ggc Gly	aag Lys	816
							act Thr 200									864
Gly 999	cca Pro 210	gcc Ala	caa Gln	aat Asn	tat Tyr	gat Asp 215	gtg Val	gca Ala	gca Ala	aat Asn	gtc Val 220	tct Ser	gag Glu	gac Asp	aac Asn	912
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cac His	ata Ile	gaa Glu	gta Val	aat Asn 245	ggt Gly	gca Ala	gat Asp	caa Gln	cct Pro 250	cca Pro	tcc Ser	act Thr	cca Pro	aaa Lys 255	ctt Leu	1008
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atg Met	tct Ser 290	gga Gly	aag Lys	gaa Glu	cgt Arg	gat Asp 295	cag Gln	gtt Val	gct Ala	gag Glu	cag Gln 300	tgc Cys	aat Asn	ttg Leu	acc Thr	1152
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		aga Arg														1440
		gat Asp														1488
		gtt Val														1536
		aag Lys 435														1584
		atg Met														1632
		aca Thr														1680
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		gac Asp														1776
		tcc Ser 515														1824
agt Ser	aag Lys 530	Gly aaa	aaa Lys	aca Thr	cat His	tca Ser 535	gct Ala	gct Ala	agt Ser	acc Thr	aaa Lys 540	tat Tyr	ggt Gly	ggt Gly	gaa Glu	1872
agc Ser 545	acc Thr	aga Arg	aat Asn	ggt Gly	cag Gln 550	aac Asn	ata Ile	cat His	gta Val	ctc Leu 555	agc Ser	gca Ala	gaa Glu	gat Asp	caa Gln 560	1920
tgc Cys	cag Gln	atg Met	gaa Glu	acc Thr 565	gaa Glu	aac Asn	tct Ser	gtt Val	ctg Leu 570	agt Ser	cac His	tcg Ser	gca Ala	aag Lys 575	gtt Val	1968

tct Ser	cca Pro	gct Ala	gag Glu 580	cat His	gat Asp	atc Ile	caa Gln	att Ile 585	Met	tct Ser	gac Asp	ctt Leu	cat His 590	gag Glu	cag Gln	2016
_			_	_	aaa Lys	_	_				_			_		2064
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					gtc Val 790											2640
					cca Pro											2688

cag gtc (Gln Val 1				Pro :									2736
agt aag	_		Arg A										2784
aaa gaa Lys Glu 8 850	_		_			_	_	_	_	-			2832
aca tta g Thr Leu 1 865	_							_			_	_	2880
gag tot (Glu Ser (2928
tca acc a	_			Ser J		_			-			_	2976
aca ttc g			Arg F										3024
tta cgc (Leu Arg 1 930													3072
gaa att g Glu Ile 2 945													3120
tta gga q Leu Gly V					_		_	_		_	_	_	3168
cat ttt q				Gly I									3216
ttg cag t Leu Gln I			Ser S					Phe					3264
aac agc a Asn Ser 1	_	Gln Ser			_		Lys			_	_		3312
ccc ttg o Pro Leu i 1025						Ile					Lys		3360
cca gct q Pro Ala A	Asp Phe				Asn					Met			3408

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Arg

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Glu Leu Thr Ala Thr Pro Arg Gln Asp Ala Ala Glu Ala Gly Val 35 40 45

Asp Glu Pro Ala Gln His Gln Cys Glu His Phe Ser Ile Arg Gly Tyr 50 60

Val Ala Leu Leu Gln Lys Lys Asp Pro Lys Phe Cys Ser Leu Ser Arg 65 70 75 80

Ile Phe His Asp Gln Lys Lys Cys Asp Glu His Lys Ala Ser Ser Ser 85 90 95

Pro Phe Ser Val Ala Lys Phe Arg Arg Trp Asp Cys Ser Lys Cys Leu 100 105 110

Asp Lys Leu Lys Thr Ser Asp Asn Gly Thr Ala Pro Arg Thr Leu Pro 115 120 125

Ala Lys Gln Asn Gly Thr Ser Asp Gly Cys Ser Ile Thr Phe Val Arg 130 135 140

Ser Thr Phe Val Pro Ala Ser Val Gly Ser Gln Lys Val Ser Pro Ser 145 150 155 160

Thr Gln Ser Ser Gln Gly Lys Asn Ala Asp Arg Ser Thr Leu Pro Lys
165 170 175

Ser Val Gln Glu Gly Asn Asp Ser Lys Cys Asn Ala Pro Ser Gly Lys 180 185 190 Asn Gly Ala Ala Glu Ala Asn Thr Asp Ser Pro Met Lys Asp Leu Gln 200 Gly Pro Ala Gln Asn Tyr Asp Val Ala Ala Asn Val Ser Glu Asp Asn 220 215 Thr Ser Val Asp Val Gly Ala Leu Pro Glu Val Pro Gln Ile Thr Trp 230 235 His Ile Glu Val Asn Gly Ala Asp Gln Pro Pro Ser Thr Pro Lys Leu 250 Ser Glu Val Val Leu Lys Arg Asn Glu Asp Glu Asn Gly Lys Thr Glu 265 Glu Thr Leu Val Ala Glu Gln Cys Asn Leu Thr Lys Asp Pro Asn Pro 275 Met Ser Gly Lys Glu Arg Asp Gln Val Ala Glu Gln Cys Asn Leu Thr 295 Lys Asp Pro Lys Pro Val Ser Gly Gln Lys Cys Glu Gln Ile Cys Asn Glu Pro Cys Glu Glu Val Val Leu Lys Arg Ser Ser Lys Ser Lys Arg 330 Lys Thr Asp Lys Lys Leu Met Lys Lys Gln Gln His Ser Lys Lys Arg Thr Ala Gln Ala Asp Val Ser Asp Ala Lys Leu Cys Arg Arg Lys Pro 360 Lys Lys Val Arg Leu Leu Ser Glu Ile Ile Asn Ala Asn Gln Val Glu 370 Asp Ser Arg Ser Asp Glu Val His Arg Glu Asn Ala Ala Asp Pro Cys 395 390 Glu Asp Asp Arg Ser Thr Ile Pro Val Pro Met Glu Val Ser Met Asp 410 Ile Pro Val Ser Asn His Thr Val Gly Glu Asp Gly Leu Lys Ser Ser 425 Lys Asn Lys Thr Lys Arg Lys Tyr Ser Asp Val Val Asp Asp Gly Ser Ser Leu Met Asn Trp Leu Asn Gly Lys Lys Lys Arg Thr Gly Ser Val His His Thr Val Ala His Pro Ala Gly Asn Leu Ser Asn Lys Lys Val Thr Pro Thr Ala Ser Thr Gln His Asp Asp Glu Asn Asp Thr Glu Asn Gly Leu Asp Thr Asn Met His Lys Thr Asp Val Cys Gln His Val Ser Glu Ile Ser Thr Gln Arg Cys Ser Ser Lys Gly Lys Thr Ala Gly Leu 520 515 Ser Lys Gly Lys Thr His Ser Ala Ala Ser Thr Lys Tyr Gly Glu 535 Ser Thr Arg Asn Gly Gln Asn Ile His Val Leu Ser Ala Glu Asp Gln 555 550 Cys Gln Met Glu Thr Glu Asn Ser Val Leu Ser His Ser Ala Lys Val 570 Ser Pro Ala Glu His Asp Ile Gln Ile Met Ser Asp Leu His Glu Gln 585 Ser Leu Pro Lys Lys Lys Lys Gln Lys Leu Glu Val Thr Arg Glu 600 Lys Gln Thr Met Ile Asp Asp Ile Pro Met Asp Ile Val Glu Leu Leu Ala Lys Asn Gln His Glu Arg Gln Leu Met Thr Glu Thr Asp Cys Ser 635 630 Asp Ile Asn Arg Ile Gln Ser Lys Thr Thr Ala Asp Asp Asp Cys Val 650 Ile Val Ala Ala Lys Asp Gly Ser Asp Tyr Ala Ser Ser Val Phe Asp 665 Thr Asn Ser Gln Gln Lys Ser Leu Ala Ser Gln Ser Thr Gln Lys Glu 680 Leu Gln Gly His Leu Ala Leu Thr Thr Gln Glu Ser Pro His Pro Gln 695 Asn Phe Gln Ser Thr Gln Glu Gln Gln Thr His Leu Arg Met Glu Glu 710 Met Val Thr Ile Ala Ala Ser Ser Pro Leu Phe Ser His His Asp Asp 730 Gln Tyr Ile Ala Glu Ala Pro Thr Glu His Trp Gly Arg Lys Asp Ala Lys Lys Leu Thr Trp Glu Gln Phe Lys Ala Thr Thr Arg Asn Ser Pro Ala Ala Thr Cys Gly Ala Gln Phe Arg Pro Gly Ile Gln Ala Val Asp Leu Thr Ser Thr His Val Met Gly Ser Ser Ser Asn Tyr Ala Ser Arg Gln Pro Val Ile Ala Pro Leu Asp Arg Tyr Ala Glu Arg Ala Val Asn 805 810 Gln Val His Ala Arg Asn Phe Pro Ser Thr Ile Ala Thr Met Glu Ala 825 820

Ser Lys Leu Cys Asp Arg Arg Asn Ala Gly Gln Val Val Leu Tyr Pro 835 840 845

Lys Glu Ser Met Pro Ala Thr His Leu Leu Arg Met Met Asp Pro Ser 850 855 860

Thr Leu Ala Ser Phe Pro Asn Tyr Gly Thr Ser Ser Arg Asn Gln Met 865 870 875 880

Glu Ser Gln Leu His Asn Ser Gln Tyr Ala His Asn Gln Tyr Lys Gly 885 890 895

Ser Thr Ser Thr Ser Tyr Gly Ser Asn Leu Asn Gly Lys Ile Pro Leu 900 905 910

Thr Phe Glu Asp Leu Ser Arg His Gln Leu His Asp Leu His Arg Pro 915 920 925

Leu Arg Pro His Pro Arg Val Gly Val Leu Gly Ser Leu Leu Gln Lys 930 935 940

Glu Ile Ala Asn Trp Ser Glu Asn Cys Gly Thr Gln Ser Gly Tyr Lys 945 950 955 960

Leu Gly Val Ser Thr Gly Ile Thr Ser His Gln Met Asn Arg Lys Glu
965 970 975

His Phe Glu Ala Leu Asn Ser Gly Met Phe Ser Ala Lys Trp Asn Ala 980 985 990

Leu Gln Leu Gly Ser Val Ser Ser Ser Ala Asp Phe Leu Ser Ala Arg
995 1000 1005

Asn Ser Ile Ala Gln Ser Trp Thr Arg Gly Lys Gly Lys Met Val His 1010 1015 1020

Pro Leu Asp Arg Phe Val Arg Gln Asp Ile Cys Ile Thr Asn Lys Asn 1025 1030 1035 1040

Pro Ala Asp Phe Thr Thr Ile Ser Asn Asp Asn Glu Tyr Met Asp Tyr 1045 1050 1055

Arg